SEQ ID NO:3; Alignment result 1.
Database; PIR_76; Ac NO:D70672

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 18, 2004, 14:12:09 ; Search time 6.5921 Seconds
(without alignments)
87.531 Million cell updates/sec

Title: US-09-643-260-3
Perfect score: 26
Sequence: 1 LDASAL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	26	100.0	84	2	D70672	hypothetical prote
2	26	100.0	129	2	T31200	hypothetical prote
3	26	100.0	130	2	F90278	conserved hypothet
4	26	100.0	171	2	F87628	hypothetical prote
5	26	100.0	230	2	E95326	AtrA transcription
6	26	100.0	259	2	F69311	conserved hypothet
7	26	100.0	281	2	C83635	hypothetical prote
8	26	100.0	334	2	T37024	probable DNA-bindi
9	26	100.0	383	2	H98287	hypothetical prote
10	26	100.0	394	2	H81807	conserved hypothet
11	26	100.0	394	2	B81062	conserved hypothet
12	26	100.0	437	2	A70587	hypothetical prote
13	26	100.0	483	2	AH3265	aspartate ammonia-
14	26	100.0	512	2	H81847	hypothetical prote
15	26	100.0	513	2	A96265	hypothetical prote
16	26	100.0	513	2	AH3019	sigma 54 dependent
17	26	100.0	516	2	E81092	hypothetical prote
18	26	100.0	550	2	H70772	probable argS prot
19	26	100.0	586	2	T49210	hypothetical prote
20	26	100.0	638	2	I39196	amiloride sensitiv
21	26	100.0	855	2	T41336	probable nitrogen
22	26	100.0	894	2	G82260	leucyl-tRNA synthe
23	26	100.0	920	2	I40614	surface array prot
24	26	100.0	1006	2	T41439	putitive sulfite r
25	26	100.0	1313	1	JC2038	peptidyl-dipeptida
26	24	92.3	58	2	S55558	allophycocyanin be
27	24	92.3	157	2	C70882	hypothetical prote
28	24	92.3	166	2	AC1940	purine-binding che
29	24	92.3	179	2	B96989	probable membrane
30	24	92.3	197	2	A64484	conserved hypothet
31	24	92.3	279	2	A83986	hypothetical prote
32	24	92.3	292	2	A95163	hypothetical prote
33	24	92.3	292	2	H98028	hypothetical prote
34	24	92.3	294	2	T26946	hypothetical prote
35	24	92.3	298	2	A41227	protein kinase (EC
36	24	92.3	304	2	T42939	hypothetical prote
37	24	92.3	326	2	T09995	phosphoprotein pho
38	24	92.3	346	1	I78840	protein kinase (EC
39	24	92.3	359	1	ADEC2A	fructose-bisphosph
40	24	92.3	359	2	D91103	fructose-bisphosph
41	24	92.3	359	2	AC0875	fructose 1,6-bisph
42	24	92.3	384	2	G85948	fructose-bisphosph
43	24	92.3	393	2	S69191	adenosylmethionine
44	24	92.3	401	2	AC2113	alanine racemase [
45	24	92.3	405	1	XUECSD	dihydrolipoamide S

ALIGNMENTS

RESULT 1
D70672
hypothetical protein Rv2975c - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: D70672
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gord
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroy
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete ge
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: D70672
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-84 <COL>
A;Cross-references: GB:Z83018; GB:AL123456; NID:g3261671; PIDN:CAB05437.1; PID:e283
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: Rv2975c

Query Match 100.0%; Score 26; DB 2; Length 84;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASAL 6
||||||
Db 8 LDASAL 13

RESULT 2
T31200
hypothetical protein 633 - Sphingomonas aromaticivorans plasmid pNL1
C;Species: Sphingomonas aromaticivorans
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000
C;Accession: T31200
R;Romine, M.F.; Stillwell, L.C.; Wong, K.K.; Thurston, S.J.; Sisk, E.C.; Sensen, C
submitted to the EMBL Data Library, July 1998
A;Description: Complete sequence of a 184 kb catabolic plasmid from Sphingomonas a
A;Reference number: Z20992
A;Accession: T31200
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-129 <ROM>
A;Cross-references: EMBL:AF079317; NID:g3378261; PID:g3378341; PIDN:AAD03924.1
C;Genetics:
A;Genome: plasmid pNL1
A;Note: orf633

Query Match 100.0%; Score 26; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 19;

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 18, 2004, 13:37:19 ; Search time 22.7763 Seconds
(without alignments)
41.814 Million cell updates/sec

Title: US-09-643-260-2
Perfect score: 40
Sequence: 1 LDWSWL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_19Jun03:*
1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
7: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*
8: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
9: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
10: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*
11: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:*
12: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*
13: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
14: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:*
15: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:*
16: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:*
17: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:*
18: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:*
19: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:*
20: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
23: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	40	100.0	6	23	ABB08725	IKKbeta NEMO bindi
2	40	100.0	6	23	AAM48530	Anti-inflammatory
3	40	100.0	6	23	AAM48655	NBD mutant peptide
4	40	100.0	6	24	ABU08418	Human NEMO binding
5	40	100.0	7	23	AAM48534	Anti-inflammatory
6	40	100.0	8	23	AAM48527	Anti-inflammatory
7	40	100.0	8	23	AAM48535	Anti-inflammatory
8	40	100.0	9	20	AAW96182	IKK-alpha polypept
9	40	100.0	9	23	AAM48526	Anti-inflammatory
10	40	100.0	9	23	AAM48529	Anti-inflammatory
11	40	100.0	9	23	AAM48532	Anti-inflammatory
12	40	100.0	9	23	AAM48533	Anti-inflammatory
13	40	100.0	10	23	ABB77313	IKKbeta NEMO bindi
14	40	100.0	10	23	AAM48528	Anti-inflammatory
15	40	100.0	10	23	AAM48531	Anti-inflammatory
16	40	100.0	11	23	ABB77311	Human NBD peptide
17	40	100.0	11	23	AAM48506	Human IKKbeta pept
18	40	100.0	11	23	AAM48525	Anti-inflammatory
19	40	100.0	11	23	AAM48653	NBD peptide. Synt
20	40	100.0	13	23	AAM48640	Anti-inflammatory
21	40	100.0	13	23	AAM48641	Anti-inflammatory
22	40	100.0	13	23	AAM48642	Anti-inflammatory
23	40	100.0	13	23	AAM48645	Anti-inflammatory
24	40	100.0	17	23	AAM48638	Anti-inflammatory
25	40	100.0	17	23	AAM48639	Anti-inflammatory
26	40	100.0	17	23	AAM48643	Anti-inflammatory
27	40	100.0	17	23	AAM48644	Anti-inflammatory
28	40	100.0	18	23	AAM48628	Anti-inflammatory
29	40	100.0	18	23	AAM48629	Anti-inflammatory
30	40	100.0	18	23	AAM48632	Anti-inflammatory
31	40	100.0	18	23	AAM48633	Anti-inflammatory
32	40	100.0	22	23	AAM48630	Anti-inflammatory
33	40	100.0	22	23	AAM48631	Anti-inflammatory
34	40	100.0	22	23	AAM48634	Anti-inflammatory
35	40	100.0	22	23	AAM48635	Anti-inflammatory
36	40	100.0	22	23	AAM48636	Anti-inflammatory
37	40	100.0	22	23	AAM48637	Anti-inflammatory
38	40	100.0	28	23	ABB08740	IKKbeta NEMO bindi
39	40	100.0	28	23	AAM48523	NBD peptide SEQ ID
40	40	100.0	28	24	ABU08434	Wild-type human NE
41	40	100.0	36	23	AAM48652	IKKbeta mutated pe
42	40	100.0	36	24	ABU08436	Human IkappaB kina
43	40	100.0	220	22	AAB94488	Human protein sequ
44	40	100.0	552	21	AAY84883	A GFP-I-kappaB kin
45	40	100.0	745	19	AAW49096	Human I-kappa-B ki

ALIGNMENTS

RESULT 1
ABB08725
ID ABB08725 standard; peptide; 6 AA.
XX
AC ABB08725;
XX
DT 14-JUN-2002 (first entry)
XX
DE IKKbeta NEMO binding domain peptide SEQ ID NO 2.
XX
KW IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
KW autoimmune disease; transplant rejection; osteoporosis; cancer;
KW Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;
KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
KW corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;
KW osteopathic; cytostatic; nootropic; neuroprotective; anti-HIV; human;
KW antiarteriosclerotic; virucide; antiasthmatic; antiallergic;
KW dermatological; antibacterial; antipsoriatic; antirheumatic;
KW antiarthritic; osteopathic; antiulcer.
XX
OS Homo sapiens.
XX
PN WO200183547-A2.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US40654.
XX
PR 02-MAY-2000; 2000US-201261P.
PR 22-AUG-2000; 2000US-0643260.
XX

PA (UYYA) UNIV YALE.
XX
PI May MJ, Ghosh S;
XX
DR WPI; 2002-179350/23.
XX
PT Modulating NF-kappaB induction in a cell, useful for treating e.g.
PT inflammatory disorders, osteoporosis and cancer, comprises contacting a
PT cell with an anti-inflammatory compound comprising at least one NEMO
PT binding domain -
XX
PS Claim 23; Page 44; 82pp; English.
XX
CC The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
CC comprises contacting a cell with an anti-inflammatory compound
CC (ABB08725-ABB08742) comprising at least one NEMO binding domain
CC (ABB77313). The compound has acts through selective inhibition of
CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO
CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
CC interaction results in inhibition of IKKbeta kinase activation and
CC subsequent decreased phosphorylation of IkappaB. The compound may also
CC act (directly or indirectly) by blocking the recruitment of leukocytes
CC into sites of acute and chronic inflammation, by down-regulating the
CC expression of E-selectin on leukocytes or by blocking osteoclast
CC differentiation. The compound is useful in treating NF-kB mediated
CC conditions, where the condition is an inflammatory disorder, an
CC autoimmune disease, transplant rejection, osteoporosis, cancer,
CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia
CC telangiectasia. The inflammatory disorder is asthma, allergies,
CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
CC bowel disease, chronic obstructive pulmonary disease, vasculitis and
CC bursitis. The inflammatory disorder may also be dermatitis, eczema,
CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and
CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,
CC polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
CC cryoglobulinaemia or multiple sclerosis. For chronic viral infections
CC caused by Epstein-barr, cytomegalovirus or herpes simplex. Other viral
CC diseases include HIV and influenza. The compound may also be useful for
CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,
CC sunburn or aging. The compound may be used to replace corticosteroids in
CC any application in which corticosteroids are used, including
CC immunosuppression in transplants and cancer therapy. Also for identifying
CC antiinflammatory compounds and for diagnosis of an inflammatory disorder.
CC The compound may be administered alone or in combination with other known
CC anti-inflammatory agents. The present sequence is that of the NEMO
CC binding domain of IKKbeta.
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 40; DB 23; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSWL 6
||||||
Db 1 LDWSWL 6

RESULT 2
AAM48530
ID AAM48530 standard; Peptide; 6 AA.
XX
AC AAM48530;
XX
DT 20-MAR-2002 (first entry)
XX
DE Anti-inflammatory peptide SEQ ID NO 33.
XX
KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX
OS Synthetic.
XX
PN WO200183554-A2.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US14346.
XX
PR 02-MAY-2000; 2000US-201261P.
PR 22-AUG-2000; 2000US-0643260.
XX
PA (PRAE-) PRAECIS PHARM INC.
PA (UYYA) UNIV YALE.
XX
PI May MJ, Ghosh S, Findeis MA, Phillips K;
XX
DR WPI; 2002-121889/16.
XX
PT Novel antiinflammatory compound comprising membrane translocation
PT domain fused to NEMO binding sequence, useful for blocking nuclear
PT factor kappaB activation, and for treating asthma, lung inflammation,
PT psoriasis -
XX
PS Claim 6; Page 61; 88pp; English.
XX
CC The invention relates to an antiinflammatory compound (especially
CC AAM48628-AAM48645), comprising a membrane translocation domain
CC (AAM48620-AMM48627 or AAM48646-AAM48651) which comprises from 6-15
CC amino acid residues, fused to a NEMO binding sequence
CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
CC antibacterial, immunosuppressive, dermatological, neuroprotective,
CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The
CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC the NEMO binding domain that results in inhibition of IKKbeta kinase
CC activation and subsequent decreased phosphorylation of IkappaB. The
CC compounds are useful for treating inflammatory disorders, e.g. asthma,
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 40; DB 23; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSWL 6
||||||
Db 1 LDWSWL 6

RESULT 3
AAM48655
ID AAM48655 standard; Peptide; 6 AA.
XX
AC AAM48655;
XX
DT 20-MAR-2002 (first entry)
XX

DE NBD mutant peptide SEQ ID NO 2.
XX
KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX
OS Synthetic.
XX
PN WO200183554-A2.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US14346.
XX
PR 02-MAY-2000; 2000US-201261P.
PR 22-AUG-2000; 2000US-0643260.
XX
PA (PRAE-) PRAECIS PHARM INC.
PA (UYYA) UNIV YALE.
XX
PI May MJ, Ghosh S, Findeis MA, Phillips K;
XX
DR WPI; 2002-121889/16.
XX
PT Novel antiinflammatory compound comprising membrane translocation
PT domain fused to NEMO binding sequence, useful for blocking nuclear
PT factor kappaB activation, and for treating asthma, lung inflammation,
PT psoriasis -
XX
PS Example 6; Page 47; 88pp; English.
XX
CC The invention relates to an antiinflammatory compound (especially
CC AAM48628-AAM48645), comprising a membrane translocation domain
CC (AAM48620-AMM48627 or AAM48646-AAM48651) which comprises from 6-15
CC amino acid residues, fused to a NEMO binding sequence
CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
CC antibacterial, immunosuppressive, dermatological, neuroprotective,
CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The
CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC the NEMO binding domain that results in inhibition of IKKbeta kinase
CC activation and subsequent decreased phosphorylation of IkappaB. The
CC compounds are useful for treating inflammatory disorders, e.g. asthma,
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 40; DB 23; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSWL 6
||||||
Db 1 LDWSWL 6

RESULT 4
ABU08418

ID ABU08418 standard; peptide; 6 AA.
XX
AC ABU08418;
XX
DT 12-JUN-2003 (first entry)
XX
DE Human NEMO binding site (NBD) mutant peptide #1.
XX
KW Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;
KW IkappaB kinase-beta; IkappaB kinase-alpha; IKKalpha; NF-kappaB;
KW nuclear factor-kappaB induction; inflammatory disorder;
KW autoimmune disease; osteoporosis; cancer; Alzheimer's disease;
KW atherosclerosis; viral infection; Ataxia telangiectasia;
KW transplantation detection; immunosuppressive; osteopathic;
KW cytostatic; nootropic; neuroprotective; antiatherosclerotic; virucide;
KW vasotropic; antirheumatic; antiarthritic; mutant; mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US2002156000-A1.
XX
PD 24-OCT-2002.
XX
PF 02-MAY-2001; 2001US-0847940.
XX
PR 02-MAY-2000; 2000US-201261P.
PR 22-AUG-2000; 2000US-0643260.
XX
PA (MAYM/) MAY M J.
PA (GHOS/) GHOSH S.
XX
PI May MJ, Ghosh S;
XX
DR WPI; 2003-209142/20.
DR N-PSDB; ABX94269, ABX94270.
XX
PT Novel antiinflammatory peptide compounds comprising NEMO binding
PT domain, useful for modulating NF-kappaB induction in a cell and for
PT treating NF-kappaB-mediated inflammation disorders e.g., asthma,
PT psoriasis, vasculitis -
XX
PS Claim 22; Page 17; 47pp; English.
XX
CC The present invention relates to antiinflammatory compounds comprising
CC NEMO binding domain (NBD) peptides. The NEMO binding domains are
CC found on IkappaB kinase-beta (IKKbeta) and IkappaB kinase-alpha
CC (IKKalpha) proteins. The antiinflammatory compounds of the invention
CC are useful for modulating nuclear factor-kappaB (NF-kappaB) induction
CC in a cell, where the compounds are capable of blocking the interaction
CC between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The
CC antiinflammatory compound further comprises at least one membrane
CC translocation domain. The compounds are useful for treating
CC inflammatory disorders, autoimmune diseases, osteoporosis, cancer,
CC Alzheimer's disease, atherosclerosis, viral infections, Ataxia
CC telangiectasia, and for transplantation detection. The compounds of
CC the invention block NF-kappaB induction by IKK but do not inhibit
CC the basal activity of NF-kappaB. ABU08418-ABU08432 represent human
CC NBD mutant peptides.
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 40; DB 24; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSWL 6
||||||
Db 1 LDWSWL 6

RESULT 5
AAM48534

ID AAM48534 standard; Peptide; 7 AA.
XX
AC AAM48534;
XX
DT 20-MAR-2002 (first entry)
XX
DE Anti-inflammatory peptide SEQ ID NO 37.
XX
KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX
OS Synthetic.
XX
PN WO200183554-A2.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US14346.
XX
PR 02-MAY-2000; 2000US-201261P.
PR 22-AUG-2000; 2000US-0643260.
XX
PA (PRAE-) PRAECIS PHARM INC.
PA (UYYA) UNIV YALE.
XX
PI May MJ, Ghosh S, Findeis MA, Phillips K;
XX
DR WPI; 2002-121889/16.
XX
PT Novel antiinflammatory compound comprising membrane translocation
PT domain fused to NEMO binding sequence, useful for blocking nuclear
PT factor kappaB activation, and for treating asthma, lung inflammation,
PT psoriasis -
XX
PS Claim 6; Page 61; 88pp; English.
XX
CC The invention relates to an antiinflammatory compound (especially
CC AAM48628-AAM48645), comprising a membrane translocation domain
CC (AAM48620-AMM48627 or AAM48646-AAM48651) which comprises from 6-15
CC amino acid residues, fused to a NEMO binding sequence
CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
CC antibacterial, immunosuppressive, dermatological, neuroprotective,
CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The
CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC the NEMO binding domain that results in inhibition of IKKbeta kinase
CC activation and subsequent decreased phosphorylation of IkappaB. The
CC compounds are useful for treating inflammatory disorders, e.g. asthma,
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.
XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 40; DB 23; Length 7;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSWL 6
Db 1 LDWSWL 6

RESULT 6
AAM48527
ID AAM48527 standard; Peptide; 8 AA.
XX
AC AAM48527;
XX
DT 20-MAR-2002 (first entry)
XX
DE Anti-inflammatory peptide SEQ ID NO 30.
XX
KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX
OS Synthetic.
XX
PN WO200183554-A2.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US14346.
XX
PR 02-MAY-2000; 2000US-201261P.
PR 22-AUG-2000; 2000US-0643260.
XX
PA (PRAE-) PRAECIS PHARM INC.
PA (UYYA) UNIV YALE.
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PI May MJ, Ghosh S, Findeis MA, Phillips K;
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DR WPI; 2002-121889/16.
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CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
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CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The
CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC the NEMO binding domain that results in inhibition of IKKbeta kinase
CC activation and subsequent decreased phosphorylation of IkappaB. The
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CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.
XX
SQ Sequence 8 AA;

```
  Query Match             100.0%;  Score 40;  DB 23;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 9.3e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LDWSWL 6
              ||||||
Db          3 LDWSWL 8


RESULT 7
AAM48535
ID   AAM48535 standard; Peptide; 8 AA.
XX
AC   AAM48535;
XX
DT   20-MAR-2002  (first entry)
XX
DE   Anti-inflammatory peptide SEQ ID NO 38.
XX
KW   Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
KW   antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW   immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW   antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KW   cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW   rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW   autoimmune disorder; multiple sclerosis; transplant rejection;
KW   osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW   ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX
OS   Synthetic.
XX
PN   WO200183554-A2.
XX
PD   08-NOV-2001.
XX
PF   02-MAY-2001; 2001WO-US14346.
XX
PR   02-MAY-2000; 2000US-201261P.
PR   22-AUG-2000; 2000US-0643260.
XX
PA   (PRAE-) PRAECIS PHARM INC.
PA   (UYYA ) UNIV YALE.
XX
PI   May MJ,  Ghosh S,  Findeis MA,  Phillips K;
XX
DR   WPI; 2002-121889/16.
XX
PT   Novel antiinflammatory compound comprising membrane translocation
PT   domain fused to NEMO binding sequence, useful for blocking nuclear
PT   factor kappaB activation, and for treating asthma, lung inflammation,
PT   psoriasis  -
XX
PS   Claim 6; Page 61; 88pp; English.
XX
CC   The invention relates to an antiinflammatory compound (especially
CC   AAM48628-AAM48645), comprising a membrane translocation domain
CC   (AAM48620-AMM48627 or AAM48646-AAM48651) which comprises from 6-15
CC   amino acid residues, fused to a NEMO binding sequence
CC   (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
CC   cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
CC   antibacterial, immunosuppressive, dermatological, neuroprotective,
CC   nootropic, antiatherosclerotic, virucide and antiallergic activity. The
CC   compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC   activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC   the NEMO binding domain that results in inhibition of IKKbeta kinase
CC   activation and subsequent decreased phosphorylation of IkappaB. The
CC   compounds are useful for treating inflammatory disorders, e.g. asthma,
CC   lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC   osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC   bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC   granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC   Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC   telangiectasia. The compounds are also useful for treating
CC   pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC   drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC   arthritis.
XX
SQ   Sequence   8 AA;

  Query Match             100.0%;  Score 40;  DB 23;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 9.3e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LDWSWL 6
              ||||||
Db          1 LDWSWL 6


RESULT 8
AAW96182
ID   AAW96182 standard; peptide; 9 AA.
XX
AC   AAW96182;
XX
DT   27-APR-1999  (first entry)
XX
DE   IKK-alpha polypeptide with binding activity.
XX
KW   I-kappa-B kinase; IKK-alpha; gene expression; modulation;
KW   suppression; activation; tumour necrosis factor; TNF; interleukin-1;
KW   IL-1; TNF receptor associated factor; TRAF.
XX
OS   Homo sapiens.
XX
PN   WO9901541-A1.
XX
PD   14-JAN-1999.
XX
PF   01-JUL-1998;   98WO-US13782.
XX
PR   10-JUL-1997;   97US-0890854.
PR   01-JUL-1997;   97US-0887115.
XX
PA   (TULA-) TULARIK INC.
XX
PI   Cao Z,  Regnier C,  Rothe M;
XX
DR   WPI; 1999-106044/09.
XX
PT   Newly isolated human kinase IkappaB Kinase (IKK-^a) polypeptides -
PT   useful in screening for agents that modulate the interaction of an
PT   IKK polypeptide to a binding target and for modulating signal
PT   transduction involving IkappaB in a cell
XX
PS   Disclosure; Page -; 32pp; English.
XX
CC   I-kappa-B kinase (AAW96158), deletion mutants of it retaining
CC   I-kappa-B kinase activity and I-kappa-B polypeptides (comprising a
CC   six residue domain of I-kappa-B containing one of Ser32 and Ser36,
CC   and a candidate agent) can be used to screen for agents that
CC   modulate the interaction of an IKK polypeptide to a binding target.
CC   The modulation of the kinase activity of IKK-alpha forms a method
CC   for modulating signal transduction involving I-kappa-B in a cell.
CC   The IKK-alpha polypeptides are useful for generating oligonucleotide
CC   primers and probes for use in the isolation of natural
CC   IKK-alpha-encoding nucleic acids. The nucleic acids are useful as
CC   translatable transcripts, hybridization probes, polymerase chain
CC   reaction (PCR) probes and primers. Their diagnostic applications
CC   include IKK-alpha hybridization probes for identifying wild-type and
CC   mutant IKK-alpha alleles in clinical and laboratory samples.
CC   Therapeutic application includes the use of IKK- alpha nucleic acids
CC   for modulating cellular expression or intracellular
CC   concentration/availability of active IKK-alpha.
CC   Catalytically inactive IKK-alpha mutants suppress NF-kappa-B
CC   activation induced by tissue necrosis factor (TNF), interleukin-1
```

CC (IL-1) stimulation, TNF receptor-associated factor (TRAF) and
CC NF-kappa-B-inducing kinase (NIK) oversuppression. Polypeptides of
CC IKK-alpha showing exemplary binding activity are described in
CC AAW96165-W96182. These peptides all comprise one of Cys30, Glu543,
CC Leu604, Thr679, Ser680, Pro684, Thr686 or Ser687 of the full length
CC IKK-alpha described in AAW96157. Deletion mutants of the invention
CC comprise at least one of these regions.
CC N.B. The present sequence is not given in the present specification
CC but is derived from the sequence given in AAW96157 as specified.
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 40; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSWL 6
||||||
Db 2 LDWSWL 7

RESULT 9
AAM48526
ID AAM48526 standard; Peptide; 9 AA.
XX
AC AAM48526;
XX
DT 20-MAR-2002 (first entry)
XX
DE Anti-inflammatory peptide SEQ ID NO 29.
XX
KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX
OS Synthetic.
XX
PN WO200183554-A2.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US14346.
XX
PR 02-MAY-2000; 2000US-201261P.
PR 22-AUG-2000; 2000US-0643260.
XX
PA (PRAE-) PRAECIS PHARM INC.
PA (UYYA) UNIV YALE.
XX
PI May MJ, Ghosh S, Findeis MA, Phillips K;
XX
DR WPI; 2002-121889/16.
XX
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PT domain fused to NEMO binding sequence, useful for blocking nuclear
PT factor kappaB activation, and for treating asthma, lung inflammation,
PT psoriasis -
XX
PS Claim 6; Page 61; 88pp; English.
XX
CC The invention relates to an antiinflammatory compound (especially
CC AAM48628-AAM48645), comprising a membrane translocation domain
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CC amino acid residues, fused to a NEMO binding sequence
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CC antibacterial, immunosuppressive, dermatological, neuroprotective,
CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The
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CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
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CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 40; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSWL 6
||||||
Db 1 LDWSWL 6

RESULT 10
AAM48529
ID AAM48529 standard; Peptide; 9 AA.
XX
AC AAM48529;
XX
DT 20-MAR-2002 (first entry)
XX
DE Anti-inflammatory peptide SEQ ID NO 32.
XX
KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX
OS Synthetic.
XX
PN WO200183554-A2.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US14346.
XX
PR 02-MAY-2000; 2000US-201261P.
PR 22-AUG-2000; 2000US-0643260.
XX
PA (PRAE-) PRAECIS PHARM INC.
PA (UYYA) UNIV YALE.
XX
PI May MJ, Ghosh S, Findeis MA, Phillips K;
XX
DR WPI; 2002-121889/16.
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XX
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CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
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CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 40; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSWL 6
||||||
Db 1 LDWSWL 6

RESULT 11
AAM48532
ID AAM48532 standard; Peptide; 9 AA.
XX
AC AAM48532;
XX
DT 20-MAR-2002 (first entry)
XX
DE Anti-inflammatory peptide SEQ ID NO 35.
XX
KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX
OS Synthetic.
XX
PN WO200183554-A2.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US14346.
XX
PR 02-MAY-2000; 2000US-201261P.
PR 22-AUG-2000; 2000US-0643260.
XX
PA (PRAE-) PRAECIS PHARM INC.
PA (UYYA) UNIV YALE.
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XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 40; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSWL 6
||||||
Db 3 LDWSWL 8

RESULT 12
AAM48533
ID AAM48533 standard; Peptide; 9 AA.
XX
AC AAM48533;
XX
DT 20-MAR-2002 (first entry)
XX
DE Anti-inflammatory peptide SEQ ID NO 36.
XX
KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX
OS Synthetic.
XX
PN WO200183554-A2.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US14346.
XX
PR 02-MAY-2000; 2000US-201261P.
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PA (PRAE-) PRAECIS PHARM INC.
PA (UYYA) UNIV YALE.
XX

PI May MJ, Ghosh S, Findeis MA, Phillips K;
XX
DR WPI; 2002-121889/16.
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PT domain fused to NEMO binding sequence, useful for blocking nuclear
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CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 40; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSWL 6
||||||
Db 2 LDWSWL 7

RESULT 13
ABB77313
ID ABB77313 standard; peptide; 10 AA.
XX
AC ABB77313;
XX
DT 14-JUN-2002 (first entry)
XX
DE IKKbeta NEMO binding domain peptide SEQ ID NO 1.
XX
KW IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
KW autoimmune disease; transplant rejection; osteoporosis; cancer;
KW Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;
KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
KW corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;
KW osteopathic; cytostatic; nootropic; neuroprotective; anti-HIV; human;
KW antiarteriosclerotic; virucide; antiasthmatic; antiallergic;
KW dermatological; antibacterial; antipsoriatic; antirheumatic;
KW antiarthritic; osteopathic; antiulcer.
XX
OS Homo sapiens.
XX
PN WO200183547-A2.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US40654.
XX
PR 02-MAY-2000; 2000US-201261P.
PR 22-AUG-2000; 2000US-0643260.
XX
PA (UYYA) UNIV YALE.
XX
PI May MJ, Ghosh S;
XX
DR WPI; 2002-179350/23.
XX
PT Modulating NF-kappaB induction in a cell, useful for treating e.g.
PT inflammatory disorders, osteoporosis and cancer, comprises contacting a
PT cell with an anti-inflammatory compound comprising at least one NEMO
PT binding domain -
XX
PS Example 4; Page -; 82pp; English.
XX
CC The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
CC comprises contacting a cell with an anti-inflammatory compound
CC (ABB08725-ABB08742) comprising at least one NEMO binding domain
CC (ABB77313). The compound has acts through selective inhibition of
CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO
CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
CC interaction results in inhibition of IKKbeta kinase activation and
CC subsequent decreased phosphorylation of IkappaB. The compound may also
CC act (directly or indirectly) by blocking the recruitment of leukocytes
CC into sites of acute and chronic inflammation, by down-regulating the
CC expression of E-selectin on leukocytes or by blocking osteoclast
CC differentiation. The compound is useful in treating NF-kB mediated
CC conditions, where the condition is an inflammatory disorder, an
CC autoimmune disease, transplant rejection, osteoporosis, cancer,
CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia
CC telangiectasia. The inflammatory disorder is asthma, allergies,
CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
CC bowel disease, chronic obstructive pulmonary disease, vasculitis and
CC bursitis. The inflammatory disorder may also be dermatitis, eczema,
CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and
CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,
CC polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
CC cryoglobulinaemia or multiple sclerosis. For chronic viral infections
CC caused by Epstein-barr, cytomegalovirus or herpes simplex. Other viral
CC diseases include HIV and influenza. The compound may also be useful for
CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,
CC sunburn or aging. The compound may be used to replace corticosteroids in
CC any application in which corticosteroids are used, including
CC immunosuppression in transplants and cancer therapy. Also for identifying
CC antiinflammatory compounds and for diagnosis of an inflammatory disorder.
CC The compound may be administered alone or in combination with other known
CC anti-inflammatory agents. The present sequence is that of the NEMO
CC binding domain of IKKbeta.
CC Note: The present sequence is not given in the specification but is
CC encoded by the polynucleotide given at GenBank Accession No. AR067807,
CC nucleotides 2203-2235.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 40; DB 23; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSWL 6
||||||
Db 3 LDWSWL 8

RESULT 14
AAM48528
ID AAM48528 standard; Peptide; 10 AA.
XX
AC AAM48528;
XX
DT 20-MAR-2002 (first entry)

XX
DE Anti-inflammatory peptide SEQ ID NO 31.
XX
KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX
OS Synthetic.
XX
PN WO200183554-A2.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US14346.
XX
PR 02-MAY-2000; 2000US-201261P.
PR 22-AUG-2000; 2000US-0643260.
XX
PA (PRAE-) PRAECIS PHARM INC.
PA (UYYA) UNIV YALE.
XX
PI May MJ, Ghosh S, Findeis MA, Phillips K;
XX
DR WPI; 2002-121889/16.
XX
PT Novel antiinflammatory compound comprising membrane translocation
PT domain fused to NEMO binding sequence, useful for blocking nuclear
PT factor kappaB activation, and for treating asthma, lung inflammation,
PT psoriasis -
XX
PS Claim 6; Page 61; 88pp; English.
XX
CC The invention relates to an antiinflammatory compound (especially
CC AAM48628-AAM48645), comprising a membrane translocation domain
CC (AAM48620-AMM48627 or AAM48646-AAM48651) which comprises from 6-15
CC amino acid residues, fused to a NEMO binding sequence
CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
CC antibacterial, immunosuppressive, dermatological, neuroprotective,
CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The
CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC the NEMO binding domain that results in inhibition of IKKbeta kinase
CC activation and subsequent decreased phosphorylation of IkappaB. The
CC compounds are useful for treating inflammatory disorders, e.g. asthma,
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 40; DB 23; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDWSWL 6
||||||
Db 2 LDWSWL 7

RESULT 15

AAM48531
ID AAM48531 standard; Peptide; 10 AA.
XX
AC AAM48531;
XX
DT 20-MAR-2002 (first entry)
XX
DE Anti-inflammatory peptide SEQ ID NO 34.
XX
KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX
OS Synthetic.
XX
PN WO200183554-A2.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US14346.
XX
PR 02-MAY-2000; 2000US-201261P.
PR 22-AUG-2000; 2000US-0643260.
XX
PA (PRAE-) PRAECIS PHARM INC.
PA (UYYA) UNIV YALE.
XX
PI May MJ, Ghosh S, Findeis MA, Phillips K;
XX
DR WPI; 2002-121889/16.
XX
PT Novel antiinflammatory compound comprising membrane translocation
PT domain fused to NEMO binding sequence, useful for blocking nuclear
PT factor kappaB activation, and for treating asthma, lung inflammation,
PT psoriasis -
XX
PS Claim 6; Page 61; 88pp; English.
XX
CC The invention relates to an antiinflammatory compound (especially
CC AAM48628-AAM48645), comprising a membrane translocation domain
CC (AAM48620-AMM48627 or AAM48646-AAM48651) which comprises from 6-15
CC amino acid residues, fused to a NEMO binding sequence
CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
CC antibacterial, immunosuppressive, dermatological, neuroprotective,
CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The
CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC the NEMO binding domain that results in inhibition of IKKbeta kinase
CC activation and subsequent decreased phosphorylation of IkappaB. The
CC compounds are useful for treating inflammatory disorders, e.g. asthma,
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 40; DB 23; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 LDWSWL 6
              ||||||
Db          3 LDWSWL 8
```

Search completed: February 18, 2004, 14:26:17
Job time : 22.7763 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 18, 2004, 14:12:09 ; Search time 6.5921 Seconds
(without alignments)
87.531 Million cell updates/sec

Title: US-09-643-260-3
Perfect score: 26
Sequence: 1 LDASAL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	26	100.0	84	2	D70672	hypothetical prote
2	26	100.0	129	2	T31200	hypothetical prote
3	26	100.0	130	2	F90278	conserved hypothet
4	26	100.0	171	2	F87628	hypothetical prote
5	26	100.0	230	2	E95326	AtrA transcription
6	26	100.0	259	2	F69311	conserved hypothet
7	26	100.0	281	2	C83635	hypothetical prote
8	26	100.0	334	2	T37024	probable DNA-bindi
9	26	100.0	383	2	H98287	hypothetical prote
10	26	100.0	394	2	H81807	conserved hypothet
11	26	100.0	394	2	B81062	conserved hypothet
12	26	100.0	437	2	A70587	hypothetical prote
13	26	100.0	483	2	AH3265	aspartate ammonia-
14	26	100.0	512	2	H81847	hypothetical prote
15	26	100.0	513	2	A96265	hypothetical prote
16	26	100.0	513	2	AH3019	sigma 54 dependent
17	26	100.0	516	2	E81092	hypothetical prote
18	26	100.0	550	2	H70772	probable argS prot
19	26	100.0	586	2	T49210	hypothetical prote
20	26	100.0	638	2	I39196	amiloride sensitiv
21	26	100.0	855	2	T41336	probable nitrogen
22	26	100.0	894	2	G82260	leucyl-tRNA synthe
23	26	100.0	920	2	I40614	surface array prot
24	26	100.0	1006	2	T41439	putitive sulfite r
25	26	100.0	1313	1	JC2038	peptidyl-dipeptida
26	24	92.3	58	2	S55558	allophycocyanin be
27	24	92.3	157	2	C70882	hypothetical prote
28	24	92.3	166	2	AC1940	purine-binding che
29	24	92.3	179	2	B96989	probable membrane
30	24	92.3	197	2	A64484	conserved hypothet
31	24	92.3	279	2	A83986	hypothetical prote
32	24	92.3	292	2	A95163	hypothetical prote
33	24	92.3	292	2	H98028	hypothetical prote
34	24	92.3	294	2	T26946	hypothetical prote
35	24	92.3	298	2	A41227	protein kinase (EC
36	24	92.3	304	2	T42939	hypothetical prote
37	24	92.3	326	2	T09995	phosphoprotein pho
38	24	92.3	346	1	I78840	protein kinase (EC
39	24	92.3	359	1	ADEC2A	fructose-bisphosph
40	24	92.3	359	2	D91103	fructose-bisphosph
41	24	92.3	359	2	AC0875	fructose 1,6-bisph
42	24	92.3	384	2	G85948	fructose-bisphosph
43	24	92.3	393	2	S69191	adenosylmethionine
44	24	92.3	401	2	AC2113	alanine racemase [
45	24	92.3	405	1	XUECSD	dihydrolipoamide S

ALIGNMENTS

RESULT 1
D70672
hypothetical protein Rv2975c - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: D70672
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; G
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Hol
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: D70672
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-84 <COL>
A;Cross-references: GB:Z83018; GB:AL123456; NID:g3261671; PIDN:CAB05437.1; PID:e
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: Rv2975c

Query Match 100.0%; Score 26; DB 2; Length 84;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASAL 6
||||||
Db 8 LDASAL 13

RESULT 2
T31200
hypothetical protein 633 - Sphingomonas aromaticivorans plasmid pNL1
C;Species: Sphingomonas aromaticivorans
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000
C;Accession: T31200
R;Romine, M.F.; Stillwell, L.C.; Wong, K.K.; Thurston, S.J.; Sisk, E.C.; Sensen,
submitted to the EMBL Data Library, July 1998
A;Description: Complete sequence of a 184 kb catabolic plasmid from Sphingomonas
A;Reference number: Z20992
A;Accession: T31200
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-129 <ROM>
A;Cross-references: EMBL:AF079317; NID:g3378261; PID:g3378341; PIDN:AAD03924.1
C;Genetics:
A;Genome: plasmid pNL1
A;Note: orf633

Query Match 100.0%; Score 26; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 19;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 LDASAL 6
              ||||||
Db          6 LDASAL 11
```

RESULT 3
F90278
conserved hypothetical protein [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C;Accession: F90278
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: F90278
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-130 <KUR>
A;Cross-references: GB:AE006641; NID:g13814439; PIDN:AAK41485.1; GSPDB:GN00155
C;Genetics:
A;Gene: SSO1243

Query Match 100.0%; Score 26; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 LDASAL 6
              ||||||
Db          8 LDASAL 13
```

RESULT 4
F87628
hypothetical protein CC3064 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: F87628
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: F87628
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-171 <STO>
A;Cross-references: GB:AE005673; NID:g13424712; PIDN:AAK25026.1; GSPDB:GN00148
C;Genetics:
A;Gene: CC3064

Query Match 100.0%; Score 26; DB 2; Length 171;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 LDASAL 6
              ||||||
Db        118 LDASAL 123
```

RESULT 5
E95326
AtrA transcription regulator [imported] - Sinorhizobium meliloti (strain 1021) magaplasm
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C;Accession: E95326
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows
.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium
A;Reference number: A95262; MUID:21396509; PMID:11481432
A;Accession: E95326
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-230 <KUR>
A;Cross-references: GB:AE006469; PIDN:AAK65175.1; PID:g14523620; GSPDB:GN00165
A;Experimental source: strain 1021, megaplasmid pSymA
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; L
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.;
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Contents: annotation
C;Genetics:
A;Gene: atrA
A;Genome: plasmid

Query Match 100.0%; Score 26; DB 2; Length 230;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 LDASAL 6
              ||||||
Db         83 LDASAL 88
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RESULT 6
F69311
conserved hypothetical protein AF0494 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 21-Jul-2000
C;Accession: F69311
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.;
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirknes
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sy
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: F69311
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-259 <KLE>
A;Cross-references: GB:AE001070; GB:AE000782; NID:g2689393; PIDN:AAB90743.1; PID
C;Superfamily: conserved hypothetical protein MTH682

Query Match 100.0%; Score 26; DB 2; Length 259;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 LDASAL 6
              ||||||
Db        149 LDASAL 154
```

RESULT 7
C83635
hypothetical protein PA0086 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: C83635
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey,
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunist
A;Reference number: A82950; MUID:20437337; PMID:10984043

A;Accession: C83635
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-281 <STO>
A;Cross-references: GB:AE004447; GB:AE004091; NID:g9945902; PIDN:AAG03476.1; GSPDB:GN001
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA0086

Query Match 100.0%; Score 26; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASAL 6
||||||
Db 79 LDASAL 84

RESULT 8
T37024
probable DNA-binding regulator - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T37024
R;Murphy, L.; Harris, D.; Thomson, N.R.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, August 1999
A;Reference number: Z21619
A;Accession: T37024
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-334 <MUR>
A;Cross-references: EMBL:AL109989; PIDN:CAB53417.1; GSPDB:GN00070; SCOEDB:SCJ12.05c
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SCJ12.05c

Query Match 100.0%; Score 26; DB 2; Length 334;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASAL 6
||||||
Db 139 LDASAL 144

RESULT 9
H98287
hypothetical protein AGR_L_2514 [imported] - Agrobacterium tumefaciens (strain C58, Cere
C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
C;Accession: H98287
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: H98287
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-383 <KUR>
A;Cross-references: GB:AE007870; PIDN:AAK89826.1; PID:g15159760; GSPDB:GN00170
C;Genetics:
A;Gene: AGR_L_2514
A;Map position: linear chromosome

Query Match 100.0%; Score 26; DB 2; Length 383;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASAL 6
||||||
Db 270 LDASAL 275

RESULT 10
H81807
conserved hypothetical protein NMA1819 [imported] - Neisseria meningitidis (strai
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C;Accession: H81807
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Raja
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: H81807
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-394 <PAR>
A;Cross-references: GB:AL162757; GB:AL157959; NID:g7380371; PIDN:CAB85044.1; PID:
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: NMA1819

Query Match 100.0%; Score 26; DB 2; Length 394;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASAL 6
||||||
Db 365 LDASAL 370

RESULT 11
B81062
conserved hypothetical protein NMB1620 [imported] - Neisseria meningitidis (strai
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C;Accession: B81062
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eis
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli,
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC
A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Accession: B81062
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-394 <TET>
A;Cross-references: GB:AE002512; GB:AE002098; NID:g7226866; PIDN:AAF41972.1; PID:
A;Experimental source: serogroup B, strain MC58
C;Genetics:
A;Gene: NMB1620

Query Match 100.0%; Score 26; DB 2; Length 394;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASAL 6
||||||
Db 365 LDASAL 370

RESULT 12
A70587
hypothetical protein Rv2370c - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: A70587
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gc
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Hol
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete

A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: A70587
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-437 <COL>
A;Cross-references: GB:Z95208; GB:AL123456; NID:g3261747; PIDN:CAB08469.1; PID:e315159;
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: Rv2370c

Query Match 100.0%; Score 26; DB 2; Length 437;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASAL 6
||||||
Db 96 LDASAL 101

RESULT 13
AH3265
aspartate ammonia-lyase (EC 4.3.1.1) [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002
C;Accession: AH3265
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Reference number: AD3252; PMID:11756688
A;Accession: AH3265
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-483 <KUR>
A;Cross-references: GB:AE008917; PIDN:AAL51291.1; PID:g17981985; GSPDB:GN00190
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEI0109
A;Map position: I
C;Superfamily: fumarate hydratase
C;Keywords: ammonia-lyase; carbon-nitrogen lyase

Query Match 100.0%; Score 26; DB 2; Length 483;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASAL 6
||||||
Db 452 LDASAL 457

RESULT 14
H81847
hypothetical protein NMA1557 [imported] - Neisseria meningitidis (strain Z2491 serogroup
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C;Accession: H81847
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: H81847
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-512 <PAR>
A;Cross-references: GB:AL162756; GB:AL157959; NID:g7380091; PIDN:CAB84784.1; PID:g738019
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: NMA1557

Query Match 100.0%; Score 26; DB 2; Length 512;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASAL 6
||||||
Db 318 LDASAL 323

RESULT 15
A96265
hypothetical protein AGR_L_2141 [imported] - Agrobacterium tumefaciens (strain C5
C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 17-Mar-2003
C;Accession: A96265
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; G
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Marke
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacter
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: A96265
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-513 <KUR>
A;Cross-references: GB:AE007870; PIDN:AAK89643.1; PID:g15159542; GSPDB:GN00170
C;Genetics:
A;Gene: AGR_L_2141
A;Map position: linear chromosome
C;Superfamily: response regulator of the NtrC type; response regulator homology;

Query Match 100.0%; Score 26; DB 2; Length 513;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASAL 6
||||||
Db 346 LDASAL 351

Search completed: February 18, 2004, 14:38:35
Job time : 8.5921 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 18, 2004, 14:09:39 ; Search time 17.3684 Seconds
(without alignments)
89.145 Million cell updates/sec

Title: US-09-643-260-3
Perfect score: 26
Sequence: 1 LDASAL 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	26	100.0	92	10	Q9AS65	Q9as65 oryza sativ
2	26	100.0	92	16	P95120	P95120 mycobacteri
3	26	100.0	129	2	O85909	O85909 sphingomona
4	26	100.0	130	17	Q97YS3	Q97ys3 sulfolobus
5	26	100.0	130	17	Q96ZN1	Q96zn1 sulfolobus
6	26	100.0	171	16	Q9A3Y6	Q9a3y6 caulobacter
7	26	100.0	174	2	Q8KLX4	Q8klx4 pseudomonas
8	26	100.0	191	16	Q9KY23	Q9ky23 streptomyce
9	26	100.0	191	16	Q9KY22	Q9ky22 streptomyce
10	26	100.0	191	16	Q8CK50	Q8ck50 streptomyce
11	26	100.0	230	16	Q92ZG8	Q92zg8 rhizobium m
12	26	100.0	237	10	Q94IZ7	Q94iz7 oryza sativ
13	26	100.0	245	3	Q9HFU7	Q9hfu7 pneumocysti
14	26	100.0	247	2	Q9XCY6	Q9xcy6 vibrio para
15	26	100.0	259	17	O29756	O29756 archaeoglob
16	26	100.0	281	16	Q9I746	Q9i746 pseudomonas
17	26	100.0	304	10	Q9ASJ7	Q9asj7 oryza sativ
18	26	100.0	334	16	Q9RI53	Q9ri53 streptomyce
19	26	100.0	349	5	Q9VR43	Q9vr43 drosophila
20	26	100.0	383	16	Q8U4W2	Q8u4w2 agrobacteri
21	26	100.0	394	16	Q9JYE3	Q9jye3 neisseria m
22	26	100.0	394	16	Q9JR41	Q9jr41 neisseria m
23	26	100.0	420	2	Q9L9M3	Q9l9m3 escherichia
24	26	100.0	437	16	O05828	O05828 mycobacteri
25	26	100.0	455	4	Q96S13	Q96s13 homo sapien
26	26	100.0	483	16	Q8YJH4	Q8yjh4 brucella me
27	26	100.0	483	16	Q8FYC6	Q8fyc6 brucella su
28	26	100.0	512	16	Q9JU05	Q9ju05 neisseria m
29	26	100.0	513	16	Q8U9G4	Q8u9g4 agrobacteri
30	26	100.0	516	16	Q9JZ08	Q9jz08 neisseria m
31	26	100.0	580	10	Q93ZS9	Q93zs9 arabidopsis
32	26	100.0	586	10	Q9LY47	Q9ly47 arabidopsis
33	26	100.0	659	16	Q8NLE7	Q8nle7 corynebacte
34	26	100.0	673	10	Q9FVG4	Q9fvg4 zea mays (m
35	26	100.0	704	4	Q8NA24	Q8na24 homo sapien
36	26	100.0	745	16	Q8NRB3	Q8nrb3 corynebacte
37	26	100.0	791	16	Q8P854	Q8p854 xanthomonas
38	26	100.0	813	5	Q9V9C6	Q9v9c6 drosophila
39	26	100.0	903	2	Q8VTF1	Q8vtf1 bacillus st
40	26	100.0	903	2	Q9KIQ5	Q9kiq5 bacillus st
41	26	100.0	920	2	Q07366	Q07366 campylobact
42	26	100.0	941	10	Q9LT97	Q9lt97 arabidopsis
43	26	100.0	953	10	Q8GZ99	Q8gz99 arabidopsis
44	26	100.0	1013	10	Q8LQ10	Q8lq10 oryza sativ
45	26	100.0	1313	11	Q9EQM9	Q9eqm9 rattus norv

ALIGNMENTS

RESULT 1
Q9AS65
ID Q9AS65 PRELIMINARY; PRT; 92 AA.
AC Q9AS65;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE P0028E10.27 protein (OJ1276_B06.22 protein).
GN P0028E10.27 OR OJ1276_B06.22.
OS Oryza sativa (Rice), and
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530, 39947;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=O.sativa; STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
RT clone:P0028E10.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=O.sativa (japonica cultivar-group); STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, BAC
RT clone:OJ1276_B06.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AP002912; BAB39923.1; -.
DR EMBL; AP003339; BAB92513.1; -.
DR Gramene; Q9AS65; -.
SQ SEQUENCE 92 AA; 9407 MW; 6DE88E32F046CD92 CRC64;

Query Match 100.0%; Score 26; DB 10; Length 92;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASAL 6

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                ||||||
Db          31 LDASAL 36


RESULT 2
P95120
ID   P95120      PRELIMINARY;      PRT;    92 AA.
AC   P95120;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein Rv2975c.
GN   RV2975C OR MT3052.1 OR MTCY349.12.
OS   Mycobacterium tuberculosis.
OC   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC   Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX   NCBI_TaxID=1773;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=H37Rv;
RX   MEDLINE=98295987; PubMed=9634230;
RA   Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA   Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
RA   Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA   Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA   Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA   Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA   Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA   Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT   "Deciphering the biology of Mycobacterium tuberculosis from the
RT   complete genome sequence.";
RL   Nature 393:537-544(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CDC 1551 / Oshkosh;
RA   Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA   Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
RA   Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
RA   Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA   Bishai W.;
RT   "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT   laboratory strains.";
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; Z83018; CAB05437.1; ALT_INIT.
DR   EMBL; AE007126; AAK47379.1; -.
DR   TIGR; MT3052.1; -.
DR   TubercuList; Rv2975c; -.
DR   InterPro; IPR001969; Aspprotease_site.
DR   PROSITE; PS00141; ASP_PROTEASE; 1.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   92 AA;  9850 MW;  50BD1AFCFCDFD253 CRC64;

  Query Match           100.0%;  Score 26;  DB 16;  Length 92;
  Best Local Similarity  100.0%;  Pred. No. 64;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LDASAL 6
                ||||||
Db         16 LDASAL 21


RESULT 3
O85909
ID   O85909      PRELIMINARY;      PRT;   129 AA.
AC   O85909;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Hypothetical 13.3 kDa protein precursor.
GN   ORF633.
OS   Sphingomonas aromaticivorans.
OG   Plasmid pNL1.
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
OC   Sphingomonadaceae; Novosphingobium.
OX   NCBI_TaxID=48935;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=F199;
RA   Romine M.F., Stillwell L.C., Wong K.-K., Thurston S.J., Sisk E.C.,
RA   Sensen C.W., Gaasterland T., Saffer J.D., Fredrickson J.K.;
RT   "Complete sequence of a 184 kb catabolic plasmid from Sphingomonas
RT   aromaticivorans strain F199.";
RL   Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF079317; AAD03924.1; -.
DR   InterPro; IPR002716; PIN.
DR   Pfam; PF01850; PIN; 1.
KW   Hypothetical protein; Plasmid; Signal.
FT   SIGNAL        1     39       POTENTIAL.
SQ   SEQUENCE   129 AA;  13287 MW;  9B6F200F1767A297 CRC64;

  Query Match           100.0%;  Score 26;  DB 2;  Length 129;
  Best Local Similarity  100.0%;  Pred. No. 93;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LDASAL 6
                ||||||
Db          6 LDASAL 11


RESULT 4
Q97YS3
ID   Q97YS3      PRELIMINARY;      PRT;   130 AA.
AC   Q97YS3;
DT   01-OCT-2001 (TrEMBLrel. 18, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein SSO1243.
GN   SSO1243.
OS   Sulfolobus solfataricus.
OC   Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC   Sulfolobus.
OX   NCBI_TaxID=2287;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 35092 / DSM 1617 / P2;
RX   MEDLINE=21332296; PubMed=11427726;
RA   She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
RA   Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
RA   De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,
RA   Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
RA   Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
RA   Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
RA   Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
RT   "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
DR   EMBL; AE006739; AAK41485.1; -.
DR   InterPro; IPR002716; PIN.
DR   InterPro; IPR006596; PINc.
DR   Pfam; PF01850; PIN; 1.
DR   SMART; SM00670; PINc; 1.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   130 AA;  15118 MW;  15F6B4A4970B9115 CRC64;

  Query Match           100.0%;  Score 26;  DB 17;  Length 130;
  Best Local Similarity  100.0%;  Pred. No. 94;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LDASAL 6
                ||||||
Db          8 LDASAL 13


RESULT 5
Q96ZN1
ID   Q96ZN1      PRELIMINARY;      PRT;   130 AA.
AC   Q96ZN1;
```

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DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Hypothetical protein ST1801.
GN   ST1801.
OS   Sulfolobus tokodaii.
OC   Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC   Sulfolobus.
OX   NCBI_TaxID=111955;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=JCM 10545 / 7;
RX   PubMed=11572479;
RA   Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
RA   Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,
RA   Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
RA   Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
RA   Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
RA   Oshima T., Kikuchi H.;
RT   "Complete genome sequence of an aerobic thermoacidophilic
RT   Crenarchaeon, Sulfolobus tokodaii strain7.";
RL   DNA Res. 8:123-140(2001).
DR   EMBL; AP000987; BAB66893.1; -.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   130 AA;  14958 MW;  4C4A5C20D664E991 CRC64;

  Query Match             100.0%;  Score 26;  DB 17;  Length 130;
  Best Local Similarity   100.0%;  Pred. No. 94;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LDASAL 6
              ||||||
Db          7 LDASAL 12


RESULT 6
Q9A3Y6
ID   Q9A3Y6      PRELIMINARY;      PRT;   171 AA.
AC   Q9A3Y6;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Hypothetical protein CC3064.
GN   CC3064.
OS   Caulobacter crescentus.
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
OC   Caulobacteraceae; Caulobacter.
OX   NCBI_TaxID=155892;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 19089 / CB15;
RX   MEDLINE=21173698; PubMed=11259647;
RA   Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA   Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA   Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA   DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA   Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA   Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
RA   Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RT   "Complete genome sequence of Caulobacter crescentus.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
DR   EMBL; AE005969; AAK25026.1; -.
DR   HSSP; P32173; 1E5K.
DR   TIGR; CC3064; -.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   171 AA;  17046 MW;  7252F45EC2E1CEAC CRC64;

  Query Match             100.0%;  Score 26;  DB 16;  Length 171;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LDASAL 6
              ||||||
Db        118 LDASAL 123


RESULT 7
Q8KLX4
ID   Q8KLX4      PRELIMINARY;      PRT;   174 AA.
AC   Q8KLX4;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   RnfB protein.
GN   RNFB.
OS   Pseudomonas stutzeri (Pseudomonas perfectomarina).
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC   Pseudomonadaceae; Pseudomonas.
OX   NCBI_TaxID=316;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A15;
RA   Desnoues N., Lin M., Guo X., Ma L., Elmerich C.;
RT   "Organisation of nif genes in Pseudomonas stutzeri A15, a rice
RT   endophyte.";
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ297529; CAD44487.1; -.
DR   InterPro; IPR001450; 4Fe4S_ferredoxin.
DR   Pfam; PF00037; fer4; 1.
DR   Pfam; PF04060; FeS; 1.
DR   PROSITE; PS00198; 4FE4S_FERREDOXIN; 2.
KW   4Fe-4S; Iron; Iron-sulfur.
SQ   SEQUENCE   174 AA;  17648 MW;  F7B95DC793FBD9D6 CRC64;

  Query Match             100.0%;  Score 26;  DB 2;  Length 174;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LDASAL 6
              ||||||
Db         91 LDASAL 96


RESULT 8
Q9KY23
ID   Q9KY23      PRELIMINARY;      PRT;   191 AA.
AC   Q9KY23;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein SCO2367.
GN   SCO2367 OR SCC8A.25C.
OS   Streptomyces coelicolor.
OC   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC   Streptomycineae; Streptomycetaceae; Streptomyces.
OX   NCBI_TaxID=1902;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A3(2);
RA   Brown S.P., Harris D.;
RL   Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A3(2);
RA   Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
RL   Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A3(2);
RX   MEDLINE=97000351; PubMed=8843436;
RA   Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,
RA   Kinashi H., Hopwood D.A.;
RT   "A set of ordered cosmids and a detailed genetic and physical map for
RT   the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL   Mol. Microbiol. 21:77-96(1996).
RN   [4]
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RP   SEQUENCE FROM N.A.
RC   STRAIN=A3(2) / M145;
RX   MEDLINE=21996410; PubMed=12000953;
RA   Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA   Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA   Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA   Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA   Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
RA   Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
RA   Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA   Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA   Hopwood D.A.;
RT   "Complete genome sequence of the model actinomycete Streptomyces
RT   coelicolor A3(2).";
RL   Nature 417:141-147(2002).
DR   EMBL; AL939112; CAB92843.1; -.
DR   InterPro; IPR003325; TerD.
DR   Pfam; PF02342; TerD; 1.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   191 AA;  20414 MW;  C280293C548F3988 CRC64;

  Query Match             100.0%;  Score 26;  DB 16;  Length 191;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
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Qy          1 LDASAL 6
              ||||||
Db         41 LDASAL 46


RESULT 9
Q9KY22
ID   Q9KY22      PRELIMINARY;      PRT;   191 AA.
AC   Q9KY22;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein SCO2368.
GN   SCO2368 OR SCC8A.26C.
OS   Streptomyces coelicolor.
OC   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC   Streptomycineae; Streptomycetaceae; Streptomyces.
OX   NCBI_TaxID=1902;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A3(2);
RA   Brown S.P., Harris D.;
RL   Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A3(2);
RA   Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
RL   Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A3(2);
RX   MEDLINE=97000351; PubMed=8843436;
RA   Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,
RA   Kinashi H., Hopwood D.A.;
RT   "A set of ordered cosmids and a detailed genetic and physical map for
RT   the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL   Mol. Microbiol. 21:77-96(1996).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A3(2) / M145;
RX   MEDLINE=21996410; PubMed=12000953;
RA   Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA   Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA   Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA   Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA   Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
RA   Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
RA   Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA   Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA   Hopwood D.A.;
RT   "Complete genome sequence of the model actinomycete Streptomyces
RT   coelicolor A3(2).";
RL   Nature 417:141-147(2002).
DR   EMBL; AL939112; CAB92844.1; -.
DR   InterPro; IPR003325; TerD.
DR   Pfam; PF02342; TerD; 1.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   191 AA;  20387 MW;  39E9C1EC8C47AA7E CRC64;

  Query Match             100.0%;  Score 26;  DB 16;  Length 191;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LDASAL 6
              ||||||
Db         41 LDASAL 46


RESULT 10
Q8CK50
ID   Q8CK50      PRELIMINARY;      PRT;   191 AA.
AC   Q8CK50;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Tellurium resistance protein.
GN   SCO0641 OR SCF56.25 OR SCF91.01.
OS   Streptomyces coelicolor.
OC   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC   Streptomycineae; Streptomycetaceae; Streptomyces.
OX   NCBI_TaxID=1902;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A3(2) / M145;
RX   MEDLINE=21996410; PubMed=12000953;
RA   Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA   Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA   Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA   Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA   Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
RA   Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
RA   Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA   Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA   Hopwood D.A.;
RT   "Complete genome sequence of the model actinomycete Streptomyces
RT   coelicolor A3(2).";
RL   Nature 417:141-147(2002).
DR   EMBL; AL939106; CAD55270.1; -.
KW   Complete proteome.
SQ   SEQUENCE   191 AA;  20180 MW;  C5998EEF8D009B5A CRC64;

  Query Match             100.0%;  Score 26;  DB 16;  Length 191;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LDASAL 6
              ||||||
Db         41 LDASAL 46


RESULT 11
Q92ZG8
ID   Q92ZG8      PRELIMINARY;      PRT;   230 AA.
AC   Q92ZG8;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   AtrA transcriptional regulator.
GN   ATRA OR RA0517 OR SMA0955.
OS   Rhizobium meliloti (Sinorhizobium meliloti).
OG   Plasmid pSymA (megaplasmid 1).
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```
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC   Rhizobiaceae; Sinorhizobium.
OX   NCBI_TaxID=382;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=1021;
RX   MEDLINE=21396509; PubMed=11481432;
RA   Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
RA   Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
RA   Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
RA   Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
RA   Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;
RT   "Nucleotide sequence and predicted functions of the entire
RT   Sinorhizobium meliloti pSymA megaplasmid.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
DR   EMBL; AE007243; AAK65175.1; -.
DR   InterPro; IPR000524; HTH_GntR.
DR   Pfam; PF00392; gntR; 1.
DR   SMART; SM00345; HTH_GNTR; 1.
DR   PROSITE; PS00043; HTH_GNTR_FAMILY; 1.
KW   Plasmid; Complete proteome.
SQ   SEQUENCE   230 AA;  25843 MW;  82DECAC87E91B94E CRC64;

  Query Match             100.0%;  Score 26;  DB 16;  Length 230;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LDASAL 6
              ||||||
Db         83 LDASAL 88


RESULT 12
Q94IZ7
ID   Q94IZ7      PRELIMINARY;      PRT;   237 AA.
AC   Q94IZ7;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   OSJNBa0038J17.13 protein.
OS   Oryza sativa (Rice).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=4530;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Nipponbare;
RA   Sasaki T., Matsumoto T., Yamamoto K.;
RT   "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, BAC
RT   clone:OSJNBa0038J17.";
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR   EMBL; AP003104; BAB55721.1; -.
DR   Gramene; Q94IZ7; -.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF00097; zf-C3HC4; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS50089; ZF_RING_2; 1.
KW   Metal-binding; Zinc; Zinc-finger.
SQ   SEQUENCE   237 AA;  23871 MW;  EA9F0F14F9B625DC CRC64;

  Query Match             100.0%;  Score 26;  DB 10;  Length 237;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LDASAL 6
              ||||||
Db         91 LDASAL 96


RESULT 13
Q9HFU7
ID   Q9HFU7      PRELIMINARY;      PRT;   245 AA.
AC   Q9HFU7;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   Ornithine decarboxylase antizyme.
GN   ANTIZYME.
OS   Pneumocystis carinii.
OC   Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes; Pneumocystidaceae;
OC   Pneumocystis.
OX   NCBI_TaxID=4754;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Ivanov I.P., Gesteland R.F., Atkins J.F.;
RT   "Antizyme expression: a subversion of triplet decoding, which is
RT   remarkably conserved by evolution, is a sensor for an autoregulatory
RT   circuit.";
RL   Nucleic Acids Res. 28:0-0(2000).
DR   EMBL; AF291574; AAG16234.1; -.
SQ   SEQUENCE   245 AA;  27677 MW;  2ED98BA35CD5EFBD CRC64;

  Query Match             100.0%;  Score 26;  DB 3;  Length 245;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LDASAL 6
              ||||||
Db         93 LDASAL 98


RESULT 14
Q9XCY6
ID   Q9XCY6      PRELIMINARY;      PRT;   247 AA.
AC   Q9XCY6;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   TonB-like protein.
GN   TONB1.
OS   Vibrio parahaemolyticus.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC   Vibrionaceae; Vibrio.
OX   NCBI_TaxID=670;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=474801;
RX   MEDLINE=99287846; PubMed=10348876;
RA   O'Malley S.M., Mouton S.L., Occhino D.A., Deanda M.T., Rashidi J.R.,
RA   Fuson K.L., Rashidi C.E., Mora M.Y., Payne S.M., Henderson D.P.;
RT   "Comparison of the heme iron utilization systems of pathogenic
RT   vibrios.";
RL   J. Bacteriol. 181:3594-3598(1999).
DR   EMBL; AF119047; AAD39909.1; -.
DR   InterPro; IPR003538; TonB.
DR   InterPro; IPR006260; TonB_C.
DR   PRINTS; PR01374; TONBPROTEIN.
DR   TIGRFAMs; TIGR01352; tonB_Cterm; 1.
SQ   SEQUENCE   247 AA;  27121 MW;  D9497117BA4D400E CRC64;

  Query Match             100.0%;  Score 26;  DB 2;  Length 247;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LDASAL 6
              ||||||
Db        210 LDASAL 215


RESULT 15
O29756
ID   O29756      PRELIMINARY;      PRT;   259 AA.
AC   O29756;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
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DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical protein AF0494.
GN   AF0494.
OS   Archaeoglobus fulgidus.
OC   Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
OC   Archaeoglobaceae; Archaeoglobus.
OX   NCBI_TaxID=2234;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX   MEDLINE=98049343; PubMed=9389475;
RA   Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA   Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
RA   Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
RA   Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA   Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA   Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
RA   Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
RA   Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
RA   Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA   Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA   Venter J.C.;
RT   "The complete genome sequence of the hyperthermophilic, sulphate-
RT   reducing archaeon Archaeoglobus fulgidus.";
RL   Nature 390:364-370(1997).
DR   EMBL; AE001070; AAB90743.1; -.
DR   TIGR; AF0494; -.
DR   InterPro; IPR001247; 3_ExoRNase.
DR   Pfam; PF01138; RNase_PH; 1.
DR   Pfam; PF03725; RNase_PH_C; 1.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   259 AA;  28646 MW;  E8289D46F9DDCCB3 CRC64;

  Query Match             100.0%;  Score 26;  DB 17;  Length 259;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LDASAL 6
              ||||||
Db        149 LDASAL 154


Search completed: February 18, 2004, 14:35:37
Job time : 20.3684 secs
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use Result 7 + 8

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OM protein - protein search, using sw model

Run on: February 18, 2004, 13:37:19 ; Search time 22.7763 Seconds
(without alignments)
41.814 Million cell updates/sec

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Sequence: 1 LDASAL 6

Scoring table: BLOSUM62
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Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	26	100.0	6	23	ABB08726	Mutated IKKbeta NE
2	26	100.0	6	23	AAM48508	NBD mutant peptide
3	26	100.0	6	24	ABU08419	Human NEMO binding
4	26	100.0	28	23	ABB08741	Mutated IKKbeta NE
5	26	100.0	28	23	AAM48524	NBD peptide SEQ ID
6	26	100.0	28	24	ABU08435	Human mutant NEMO
7	26	100.0	84	20	AAY04950	Mycobacterium spec
8	26	100.0	92	20	AAY04947	Mycobacterium spec
9	26	100.0	102	20	AAY04951	Mycobacterium spec
10	26	100.0	102	21	AAG35536	Arabidopsis thalia
11	26	100.0	138	22	AAO01907	Human polypeptide
12	26	100.0	143	21	AAG35535	Arabidopsis thalia
13	26	100.0	160	21	AAG35534	Arabidopsis thalia
14	26	100.0	240	22	AAG90584	C glutamicum prote
15	26	100.0	271	21	AAG51025	Arabidopsis thalia
16	26	100.0	284	21	AAG51024	Arabidopsis thalia
17	26	100.0	349	22	ABB70854	Drosophila melanog
18	26	100.0	393	24	ABP77254	N. gonorrhoeae ami
19	26	100.0	462	21	AAY75181	Neisseria meningit
20	26	100.0	516	21	AAY75180	Neisseria gonorrhe
21	26	100.0	516	21	AAY75182	Neisseria meningit
22	26	100.0	516	21	AAY75183	Neisseria meningit
23	26	100.0	520	24	ABP78709	N. gonorrhoeae ami
24	26	100.0	528	22	AAU41302	Propionibacterium
25	26	100.0	564	21	AAG41649	Arabidopsis thalia
26	26	100.0	572	20	AAY04954	Mycobacterium spec
27	26	100.0	577	21	AAG41648	Arabidopsis thalia
28	26	100.0	600	22	AAU71915	C. glutamicum meta
29	26	100.0	600	22	AAB79747	Corynebacterium gl
30	26	100.0	600	22	AAB79991	Corynebacterium gl
31	26	100.0	600	22	AAB80012	Corynebacterium gl
32	26	100.0	638	24	AAO16363	Human epithelial c
33	26	100.0	659	22	AAG93061	C glutamicum prote
34	26	100.0	669	22	AAE10335	Human transporter
35	26	100.0	745	22	AAU71914	C. glutamicum meta
36	26	100.0	745	22	AAG91007	C glutamicum prote
37	26	100.0	745	22	AAB79746	Corynebacterium gl
38	26	100.0	745	22	AAB79990	Corynebacterium gl
39	26	100.0	745	22	AAB80011	Corynebacterium gl
40	26	100.0	745	23	AAM51073	Corynebacterium gl
41	26	100.0	813	22	ABB59333	Drosophila melanog
42	26	100.0	941	23	ABB93761	Herbicidally activ
43	26	100.0	967	22	AAU39591	Propionibacterium
44	26	100.0	1700	22	ABG99873	S. cinnamonensis M
45	24	92.3	14	21	AAY98392	Alpha D peptide de

ALIGNMENTS

RESULT 1
ABB08726
ID ABB08726 standard; peptide; 6 AA.
XX
AC ABB08726;
XX
DT 14-JUN-2002 (first entry)
XX
DE Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 3.
XX
KW IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
KW autoimmune disease; transplant rejection; osteoporosis; cancer;
KW Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;
KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
KW corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;
KW osteopathic; cytostatic; nootropic; neuroprotective; anti-HIV; human;
KW antiarteriosclerotic; virucide; antiasthmatic; antiallergic;
KW dermatological; antibacterial; antipsoriatic; antirheumatic;
KW antiarthritic; osteopathic; antiulcer; mutant; mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 3
FT /note= "Wildtype Trp substituted by Ala"
FT Misc-difference 5
FT /note= "Wildtype Trp substituted by Ala"
XX
PN WO200183547-A2.
XX

PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US40654.
XX
PR 02-MAY-2000; 2000US-201261P.
PR 22-AUG-2000; 2000US-0643260.
XX
PA (UYYA) UNIV YALE.
XX
PI May MJ, Ghosh S;
XX
DR WPI; 2002-179350/23.
XX
PT Modulating NF-kappaB induction in a cell, useful for treating e.g.
PT inflammatory disorders, osteoporosis and cancer, comprises contacting a
PT cell with an anti-inflammatory compound comprising at least one NEMO
PT binding domain -
XX
PS Claim 23; Page 44; 82pp; English.
XX
CC The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
CC comprises contacting a cell with an anti-inflammatory compound
CC (ABB08725-ABB08742) comprising at least one NEMO binding domain
CC (ABB77313). The compound has acts through selective inhibition of
CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO
CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
CC interaction results in inhibition of IKKbeta kinase activation and
CC subsequent decreased phosphorylation of IkappaB. The compound may also
CC act (directly or indirectly) by blocking the recruitment of leukocytes
CC into sites of acute and chronic inflammation, by down-regulating the
CC expression of E-selectin on leukocytes or by blocking osteoclast
CC differentiation. The compound is useful in treating NF-kB mediated
CC conditions, where the condition is an inflammatory disorder, an
CC autoimmune disease, transplant rejection, osteoporosis, cancer,
CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia
CC telangiectasia. The inflammatory disorder is asthma, allergies,
CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
CC bowel disease, chronic obstructive pulmonary disease, vasculitis and
CC bursitis. The inflammatory disorder may also be dermatitis, eczema,
CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and
CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,
CC polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
CC cryoglobulinaemia or multiple sclerosis. For chronic viral infections
CC caused by Epstein-barr, cytomegalovirus or herpes simplex. Other viral
CC diseases include HIV and influenza. The compound may also be useful for
CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,
CC sunburn or aging. The compound may be used to replace corticosteroids in
CC any application in which corticosteroids are used, including
CC immunosuppression in transplants and cancer therapy. Also for identifying
CC antiinflammatory compounds and for diagnosis of an inflammatory disorder.
CC The compound may be administered alone or in combination with other known
CC anti-inflammatory agents. The present sequence is that of a mutated NEMO
CC binding domain of IKKbeta.
XX
SQ Sequence 6 AA;

```
  Query Match             100.0%;  Score 26;  DB 23;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 9.3e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LDASAL 6
              ||||||
Db          1 LDASAL 6
```

RESULT 2
AAM48508
ID AAM48508 standard; Peptide; 6 AA.
XX
AC AAM48508;
XX
DT 20-MAR-2002 (first entry)
XX
DE NBD mutant peptide SEQ ID NO 3.
XX
KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX
OS Synthetic.
XX
PN WO200183554-A2.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US14346.
XX
PR 02-MAY-2000; 2000US-201261P.
PR 22-AUG-2000; 2000US-0643260.
XX
PA (PRAE-) PRAECIS PHARM INC.
PA (UYYA) UNIV YALE.
XX
PI May MJ, Ghosh S, Findeis MA, Phillips K;
XX
DR WPI; 2002-121889/16.
XX
PT Novel antiinflammatory compound comprising membrane translocation
PT domain fused to NEMO binding sequence, useful for blocking nuclear
PT factor kappaB activation, and for treating asthma, lung inflammation,
PT psoriasis -
XX
PS Example 6; Page 47; 88pp; English.
XX
CC The invention relates to an antiinflammatory compound (especially
CC AAM48628-AAM48645), comprising a membrane translocation domain
CC (AAM48620-AMM48627 or AAM48646-AAM48651) which comprises from 6-15
CC amino acid residues, fused to a NEMO binding sequence
CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
CC antibacterial, immunosuppressive, dermatological, neuroprotective,
CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The
CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC the NEMO binding domain that results in inhibition of IKKbeta kinase
CC activation and subsequent decreased phosphorylation of IkappaB. The
CC compounds are useful for treating inflammatory disorders, e.g. asthma,
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.
XX
SQ Sequence 6 AA;

```
  Query Match             100.0%;  Score 26;  DB 23;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 9.3e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LDASAL 6
              ||||||
Db          1 LDASAL 6
```

RESULT 3

```
ABU08419
ID   ABU08419 standard; peptide; 6 AA.
XX
AC   ABU08419;
XX
DT   12-JUN-2003  (first entry)
XX
DE   Human NEMO binding site (NBD) mutant peptide #2.
XX
KW   Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;
KW   IkappaB kinase-beta; IkappaB kinase-alpha; IKKalpha; NF-kappaB;
KW   nuclear factor-kappaB induction; inflammatory disorder;
KW   autoimmune disease; osteoporosis; cancer; Alzheimer's disease;
KW   atherosclerosis; viral infection; Ataxia telangiectasia;
KW   transplantation detection; immunosuppressive; osteopathic;
KW   cytostatic; nootropic; neuroprotective; antiatherosclerotic; virucide;
KW   vasotropic; antirheumatic; antiarthritic; mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   US2002156000-A1.
XX
PD   24-OCT-2002.
XX
PF   02-MAY-2001; 2001US-0847940.
XX
PR   02-MAY-2000; 2000US-201261P.
PR   22-AUG-2000; 2000US-0643260.
XX
PA   (MAYM/) MAY M J.
PA   (GHOS/) GHOSH S.
XX
PI   May MJ,  Ghosh S;
XX
DR   WPI; 2003-209142/20.
XX
PT   Novel antiinflammatory peptide compounds comprising NEMO binding
PT   domain, useful for modulating NF-kappaB induction in a cell and for
PT   treating NF-kappaB-mediated inflammation disorders e.g., asthma,
PT   psoriasis, vasculitis -
XX
PS   Claim 22; Page 17; 47pp; English.
XX
CC   The present invention relates to antiinflammatory compounds comprising
CC   NEMO binding domain (NBD) peptides. The NEMO binding domains are
CC   found on IkappaB kinase-beta (IKKbeta) and IkappaB kinase-alpha
CC   (IKKalpha) proteins. The antiinflammatory compounds of the invention
CC   are useful for modulating nuclear factor-kappaB (NF-kappaB) induction
CC   in a cell, where the compounds are capable of blocking the interaction
CC   between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The
CC   antiinflammatory compound further comprises at least one membrane
CC   translocation domain. The compounds are useful for treating
CC   inflammatory disorders, autoimmune diseases, osteoporosis, cancer,
CC   Alzheimer's disease, atherosclerosis, viral infections, Ataxia
CC   telangiectasia, and for transplantation detection. The compounds of
CC   the invention block NF-kappaB induction by IKK but do not inhibit
CC   the basal activity of NF-kappaB. ABU08418-ABU08432 represent human
CC   NBD mutant peptides.
XX
SQ   Sequence   6 AA;

  Query Match             100.0%;  Score 26;  DB 24;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 9.3e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LDASAL 6
              ||||||
Db          1 LDASAL 6


RESULT 4
ABB08741
ID   ABB08741 standard; peptide; 28 AA.
XX
AC   ABB08741;
XX
DT   14-JUN-2002  (first entry)
XX
DE   Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 19.
XX
KW   IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
KW   kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
KW   autoimmune disease; transplant rejection; osteoporosis; cancer;
KW   Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;
KW   rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
KW   corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;
KW   osteopathic; cytostatic; nootropic; neuroprotective; anti-HIV; human;
KW   antiarteriosclerotic; virucide; antiasthmatic; antiallergic;
KW   dermatological; antibacterial; antipsoriatic; antirheumatic;
KW   antiarthritic; osteopathic; antiulcer; mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 22
FT                   /note= "Wildtype Trp substituted by Ala"
FT   Misc-difference 24
FT                   /note= "Wildtype Trp substituted by Ala"
XX
PN   WO200183547-A2.
XX
PD   08-NOV-2001.
XX
PF   02-MAY-2001; 2001WO-US40654.
XX
PR   02-MAY-2000; 2000US-201261P.
PR   22-AUG-2000; 2000US-0643260.
XX
PA   (UYYA ) UNIV YALE.
XX
PI   May MJ,  Ghosh S;
XX
DR   WPI; 2002-179350/23.
XX
PT   Modulating NF-kappaB induction in a cell, useful for treating e.g.
PT   inflammatory disorders, osteoporosis and cancer, comprises contacting a
PT   cell with an anti-inflammatory compound comprising at least one NEMO
PT   binding domain  -
XX
PS   Claim 23; Fig 5; 82pp; English.
XX
CC   The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
CC   comprises contacting a cell with an anti-inflammatory compound
CC   (ABB08725-ABB08742) comprising at least one NEMO binding domain
CC   (ABB77313). The compound has acts through selective inhibition of
CC   cytokine-mediated NF-kB activation by blocking the interaction of NEMO
CC   with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO
CC   interaction results in inhibition of IKKbeta kinase activation and
CC   subsequent decreased phosphorylation of IkappaB. The compound may also
CC   act (directly or indirectly) by blocking the recruitment of leukocytes
CC   into sites of acute and chronic inflammation, by down-regulating the
CC   expression of E-selectin on leukocytes or by blocking osteoclast
CC   differentiation. The compound is useful in treating NF-kB mediated
CC   conditions, where the condition is an inflammatory disorder, an
CC   autoimmune disease, transplant rejection, osteoporosis, cancer,
CC   Alzheimer's disease, atherosclerosis, a viral infection or ataxia
CC   telangiectasia. The inflammatory disorder is asthma, allergies,
CC   urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,
CC   rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory
CC   bowel disease, chronic obstructive pulmonary disease, vasculitis and
CC   bursitis. The inflammatory disorder may also be dermatitis, eczema,
CC   psoriasis, osteoarthritis, psoriatic arthritis, lupus and
CC   spondylarthritis. Also for Crohn's disease, ulcerative colitis,
CC   polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
```

CC cryoglobulinaemia or multiple sclerosis. For chronic viral infections
CC caused by Epstein-barr, cytomegalovirus or herpes simplex. Other viral
CC diseases include HIV and influenza. The compound may also be useful for
CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,
CC sunburn or aging. The compound may be used to replace corticosteroids in
CC any application in which corticosteroids are used, including
CC immunosuppression in transplants and cancer therapy. Also for identifying
CC antiinflammatory compounds and for diagnosis of an inflammatory disorder.
CC The compound may be administered alone or in combination with other known
CC anti-inflammatory agents. The present sequence is that of a mutated NEMO
CC binding domain of IKKbeta.
XX
SQ Sequence 28 AA;

Query Match 100.0%; Score 26; DB 23; Length 28;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASAL 6
||||||
Db 20 LDASAL 25

RESULT 5
AAM48524
ID AAM48524 standard; Peptide; 28 AA.
XX
AC AAM48524;
XX
DT 20-MAR-2002 (first entry)
XX
DE NBD peptide SEQ ID NO 19.
XX
KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX
OS Synthetic.
XX
PN WO200183554-A2.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US14346.
XX
PR 02-MAY-2000; 2000US-201261P.
PR 22-AUG-2000; 2000US-0643260.
XX
PA (PRAE-) PRAECIS PHARM INC.
PA (UYYA) UNIV YALE.
XX
PI May MJ, Ghosh S, Findeis MA, Phillips K;
XX
DR WPI; 2002-121889/16.
XX
PT Novel antiinflammatory compound comprising membrane translocation
PT domain fused to NEMO binding sequence, useful for blocking nuclear
PT factor kappaB activation, and for treating asthma, lung inflammation,
PT psoriasis -
XX
PS Example 5; Fig 5; 88pp; English.
XX
CC The invention relates to an antiinflammatory compound (especially
CC AAM48628-AAM48645), comprising a membrane translocation domain
CC (AAM48620-AMM48627 or AAM48646-AAM48651) which comprises from 6-15
CC amino acid residues, fused to a NEMO binding sequence
CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
CC antibacterial, immunosuppressive, dermatological, neuroprotective,
CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The
CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC the NEMO binding domain that results in inhibition of IKKbeta kinase
CC activation and subsequent decreased phosphorylation of IkappaB. The
CC compounds are useful for treating inflammatory disorders, e.g. asthma,
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.
XX
SQ Sequence 28 AA;

Query Match 100.0%; Score 26; DB 23; Length 28;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASAL 6
||||||
Db 20 LDASAL 25

RESULT 6
ABU08435
ID ABU08435 standard; peptide; 28 AA.
XX
AC ABU08435;
XX
DT 12-JUN-2003 (first entry)
XX
DE Human mutant NEMO binding site (NBD) peptide.
XX
KW Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;
KW IkappaB kinase-beta; IkappaB kinase-alpha; IKKalpha; NF-kappaB;
KW nuclear factor-kappaB induction; inflammatory disorder;
KW autoimmune disease; osteoporosis; cancer; Alzheimer's disease;
KW atherosclerosis; viral infection; Ataxia telangiectasia;
KW transplantation detection; immunosuppressive; osteopathic;
KW cytostatic; nootropic; neuroprotective; antiatherosclerotic; virucide;
KW vasotropic; antirheumatic; antiarthritic; mutant; mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US2002156000-A1.
XX
PD 24-OCT-2002.
XX
PF 02-MAY-2001; 2001US-0847940.
XX
PR 02-MAY-2000; 2000US-201261P.
PR 22-AUG-2000; 2000US-0643260.
XX
PA (MAYM/) MAY M J.
PA (GHOS/) GHOSH S.
XX
PI May MJ, Ghosh S;
XX
DR WPI; 2003-209142/20.
XX
PT Novel antiinflammatory peptide compounds comprising NEMO binding
PT domain, useful for modulating NF-kappaB induction in a cell and for
PT treating NF-kappaB-mediated inflammation disorders e.g., asthma,
PT psoriasis, vasculitis -
XX
PS Claim 22; Fig 5A; 47pp; English.

```
XX
CC   The present invention relates to antiinflammatory compounds comprising
CC   NEMO binding domain (NBD) peptides. The NEMO binding domains are
CC   found on IkappaB kinase-beta (IKKbeta) and IkappaB kinase-alpha
CC   (IKKalpha) proteins. The antiinflammatory compounds of the invention
CC   are useful for modulating nuclear factor-kappaB (NF-kappaB) induction
CC   in a cell, where the compounds are capable of blocking the interaction
CC   between one or more IKKs such as IKKalpha or IKKbeta, and NEMO. The
CC   antiinflammatory compound further comprises at least one membrane
CC   translocation domain. The compounds are useful for treating
CC   inflammatory disorders, autoimmune diseases, osteoporosis, cancer,
CC   Alzheimer's disease, atherosclerosis, viral infections, Ataxia
CC   telangiectasia, and for transplantation detection. The compounds of
CC   the invention block NF-kappaB induction by IKK but do not inhibit
CC   the basal activity of NF-kappaB. The present sequence represents
CC   a human mutant NBD peptide.
XX
SQ   Sequence   28 AA;

  Query Match             100.0%;  Score 26;  DB 24;  Length 28;
  Best Local Similarity   100.0%;  Pred. No. 19;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LDASAL 6
              ||||||
Db         20 LDASAL 25


RESULT 7
AAY04950
ID   AAY04950 standard; Protein; 84 AA.
XX
AC   AAY04950;
XX
DT   06-JUL-1999  (first entry)
XX
DE   Mycobacterium species protein sequence 41D.
XX
KW   Secreted protein; Mycobacterium; primer; PCR; amplification; probe;
KW   hybridisation; detection; vaccine; immunisation; infection.
XX
OS   Mycobacterium sp.
XX
PN   WO9909186-A2.
XX
PD   25-FEB-1999.
XX
PF   14-AUG-1998;   98WO-FR01813.
XX
PR   11-SEP-1997;   97FR-0011325.
PR   14-AUG-1997;   97FR-0010404.
XX
PA   (INSP ) INST PASTEUR.
XX
PI   Gicquel B,  Lim EM,  Pelicic V,  Portnoi D,  Goguet de la Salmoniere Y;
PI   Guigueno A;
XX
DR   WPI; 1999-181045/15.
DR   N-PSDB; AAX34203.
XX
PT   Mycobacterial DNA vectors containing reporter constructs - for
PT   identifying coding or promoter sequences involved in
PT   infection-associated protein expression
XX
PS   Claim 32; Fig 41D; 309pp; French.
XX
CC   Sequences AAY04742-Y05000 and AAY07201-Y07204 represent secreted
CC   proteins from various Mycobacterium species microorganisms.  The
CC   encoding nucleotide sequences can be used as primers and probes for
CC   methods for detecting and identifying mycobacteria, especially belonging
CC   to the M. tuberculosis complex.  The encoded proteins can be used in
CC   vaccines for immunisation against a bacterial or viral infection.
XX
SQ   Sequence   84 AA;

  Query Match             100.0%;  Score 26;  DB 20;  Length 84;
  Best Local Similarity   100.0%;  Pred. No. 66;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LDASAL 6
              ||||||
Db          8 LDASAL 13


RESULT 8
AAY04947
ID   AAY04947 standard; Protein; 92 AA.
XX
AC   AAY04947;
XX
DT   06-JUL-1999  (first entry)
XX
DE   Mycobacterium species protein sequence 41A.
XX
KW   Secreted protein; Mycobacterium; primer; PCR; amplification; probe;
KW   hybridisation; detection; vaccine; immunisation; infection.
XX
OS   Mycobacterium sp.
XX
PN   WO9909186-A2.
XX
PD   25-FEB-1999.
XX
PF   14-AUG-1998;   98WO-FR01813.
XX
PR   11-SEP-1997;   97FR-0011325.
PR   14-AUG-1997;   97FR-0010404.
XX
PA   (INSP ) INST PASTEUR.
XX
PI   Gicquel B,  Lim EM,  Pelicic V,  Portnoi D,  Goguet de la Salmoniere Y;
PI   Guigueno A;
XX
DR   WPI; 1999-181045/15.
DR   N-PSDB; AAX34200.
XX
PT   Mycobacterial DNA vectors containing reporter constructs - for
PT   identifying coding or promoter sequences involved in
PT   infection-associated protein expression
XX
PS   Claim 32; Fig 41A; 309pp; French.
XX
CC   Sequences AAY04742-Y05000 and AAY07201-Y07204 represent secreted
CC   proteins from various Mycobacterium species microorganisms.  The
CC   encoding nucleotide sequences can be used as primers and probes for
CC   methods for detecting and identifying mycobacteria, especially belonging
CC   to the M. tuberculosis complex.  The encoded proteins can be used in
CC   vaccines for immunisation against a bacterial or viral infection.
XX
SQ   Sequence   92 AA;

  Query Match             100.0%;  Score 26;  DB 20;  Length 92;
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Qy          1 LDASAL 6
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Db         77 LDASAL 82


RESULT 9
AAY04951
ID   AAY04951 standard; Protein; 102 AA.
XX
AC   AAY04951;
XX
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DT 06-JUL-1999 (first entry)
XX
DE Mycobacterium species protein sequence 41F.
XX
KW Secreted protein; Mycobacterium; primer; PCR; amplification; probe;
KW hybridisation; detection; vaccine; immunisation; infection.
XX
OS Mycobacterium sp.
XX
PN WO9909186-A2.
XX
PD 25-FEB-1999.
XX
PF 14-AUG-1998; 98WO-FR01813.
XX
PR 11-SEP-1997; 97FR-0011325.
PR 14-AUG-1997; 97FR-0010404.
XX
PA (INSP) INST PASTEUR.
XX
PI Gicquel B, Lim EM, Pelicic V, Portnoi D, Goguet de la Salmoniere Y;
PI Guigueno A;
XX
DR WPI; 1999-181045/15.
DR N-PSDB; AAX34204.
XX
PT Mycobacterial DNA vectors containing reporter constructs - for
PT identifying coding or promoter sequences involved in
PT infection-associated protein expression
XX
PS Claim 32; Fig 41F; 309pp; French.
XX
CC Sequences AAY04742-Y05000 and AAY07201-Y07204 represent secreted
CC proteins from various Mycobacterium species microorganisms. The
CC encoding nucleotide sequences can be used as primers and probes for
CC methods for detecting and identifying mycobacteria, especially belonging
CC to the M. tuberculosis complex. The encoded proteins can be used in
CC vaccines for immunisation against a bacterial or viral infection.
XX
SQ Sequence 102 AA;

Query Match 100.0%; Score 26; DB 20; Length 102;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASAL 6
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Db 26 LDASAL 31

RESULT 10
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ID AAG35536 standard; Protein; 102 AA.
XX
AC AAG35536;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 43425.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
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PR 29-OCT-1999; 99US-0162142.

Query Match 100.0%; Score 26; DB 21; Length 102;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 LDASAL 6
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Db         63 LDASAL 68
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RESULT 11
AAO01907
ID AAO01907 standard; Protein; 138 AA.
XX
AC AAO01907;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 15799.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation.
XX
OS Homo sapiens.
XX
PN WO200164835-A2.
XX
PD 07-SEP-2001.
XX
PF 26-FEB-2001; 2001WO-US04927.
XX
PR 28-FEB-2000; 2000US-0515126.
PR 18-MAY-2000; 2000US-0577409.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX

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DR   WPI; 2001-514838/56.
DR   N-PSDB; AAI81838.
XX
PT   Isolated nucleic acids and polypeptides, useful for preventing
PT   diagnosing and treating e.g. leukaemia, inflammation and immune
PT   disorders -
XX
PS   Claim 20; SEQ ID NO 15799; 1399pp + Sequence Listing; English.
XX
CC   The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC   the encoded proteins (AA000010-AA013910) that exhibit activity elating to
CC   cytokine, cell proliferation or cell differentiation or which may induce
CC   production of other cytokines in other cell populations. The
CC   polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC   peptide therapy. The polypeptides have various cytokine-like activities,
CC   e.g. stem cell growth factor activity, haematopoiesis regulating
CC   activity, tissue growth factor activity, immunomodulatory activity and
CC   activin/inhibin activity and may be useful in the diagnosis and/or
CC   treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC   inflammation.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   138 AA;

  Query Match             100.0%;  Score 26;  DB 22;  Length 138;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LDASAL 6
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Db         54 LDASAL 59


RESULT 12
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ID   AAG35535 standard; Protein; 143 AA.
XX
AC   AAG35535;
XX
DT   18-OCT-2000  (first entry)
XX
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 43424.
XX
KW   Protein identification; signal transduction pathway; metabolic pathway;
KW   hybridisation assay; genetic mapping; gene expression control; promoter;
KW   termination sequence.
XX
OS   Arabidopsis thaliana.
XX
PN   EP1033405-A2.
XX
PD   06-SEP-2000.
XX
PF   25-FEB-2000; 2000EP-0301439.
XX
PR   25-FEB-1999;   99US-0121825.
PR   05-MAR-1999;   99US-0123180.
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PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 100.0%; Score 26; DB 21; Length 143;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASAL 6
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Db 104 LDASAL 109

RESULT 13
AAG35534
ID AAG35534 standard; Protein; 160 AA.
XX
AC AAG35534;
XX
DT 18-OCT-2000 (first entry)
XX
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KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
PI Tateishi N, Senoh A, Ikeda M, Ozaki A;
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DR WPI; 2001-376931/40.
DR N-PSDB; AAH65803.
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PT Novel polynucleotides derived from Coryneform bacteria, for identifying
PT mutation point of a gene, measuring expression of a gene, analysing
PT expression profile or pattern of a gene and identifying homologous gene
PT -
XX
PS Claim 17; SEQ ID NO: 4338; 246pp + Sequence Listing; English.
XX
CC The present invention provides a number of nucleotide and protein
CC sequences from the Coryneform bacterium Corynebacterium glutamicum. These
CC are useful for identifying the mutation point of a gene derived from a
CC mutant of coryneform bacterium, measuring expression amount and
CC analysing the expression profile or expression pattern of a gene derived
CC from Coryneform bacterium, and identifying a homologue of a gene derived
CC from coryneform bacterium. Coryneform bacteria are useful for producing
CC amino acids, nucleic acids, vitamins, saccharides and organic acids,
CC particularly L-lysine. The present sequence is a protein described
CC in the exemplification of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from the
CC European Patent Office.
XX
SQ Sequence 240 AA;

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KW hybridisation assay; genetic mapping; gene expression control; promoter;
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Job time : 23.7763 secs